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L2: Entry 7 of 17

File: USPT

Jan 27, 1998

DOCUMENT-IDENTIFIER: US 5712142 A
TITLE: Method for increasing thermostability in cellulase enzymes

Brief Summary Text (6):

The cellulase complex produced by this organism is known to contain several different cellulase enzymes with maximal activities at temperatures of 75.degree. C. to 83.degree. C. These cellulases are resistant to inhibition from cellobiose, an end product of the reactions catalyzed by cellulase. Also, the cellulases from Acidothermus cellulolyticus are active over a broad pH range centered about pH 6. A high molecular weight cellulase isolated from growth broths of Acidothermus cellulolyticus was found to have a molecular weight of approximately 156,600 to 203,400 daltons by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). This enzyme is described in U.S. Pat. No. 5,110,735.

Brief Summary Text (7):

A novel cellulase enzyme, known as the E1 endoglucanase, also secreted by Acidothermus cellulolyticus into the growth medium, is described in detail in U.S. Pat. No. 5,275,944. In its native form, this endoglucanase demonstrates a temperature optimum of 83.degree. C. and a specific activity of 40 .mu.mole glucose release from carboxymethylcellulose/min/mg protein. This E1 endoglucanase was further identified as having an isoelectric pH of 6.7. It is this E1 endoglucanase which has been modified and made the subject of this patent application. The E1 endoglucanase is a multidomain cellulase having a catalytic domain and a cellulose binding domain connected to the catalytic domain by a linker peptide.

Detailed Description Text (15):

P. pastoris has been shown to be a useful host organism for expression of large quantities of diverse heterologous proteins. P. pastoris was used to express large quantities of active full size E1.

Detailed Description Text (39):

Mutagenized DNA was transformed into E. coli strain ES1301. Transformants were screened for resistance to ampicillin and sensitivity to tetracycline in order to identify clones carrying the putatively mutagenized E1 gene. Many ampicillin-resistant candidate clones were subsequently screened on plates containing 1 mM 4-methylumbelliferyl-.beta.-D-cellobioside (MUC) to verify expression of active E1. Plasmid DNA was prepared from several clones and employed as templates in dideoxy DNA sequencing reactions using the Sequenase.RTM. kit (U.S. Biochemical, Cleveland, Ohio) to verify the sequence of E1 DNA in the region of the intended mutation. The mutated sequence was detected in every clone which was sequenced. One of these clones was selected and designated pYCC101. Each of the successfully mutated clones expresses a protein not present in control cells and which migrates at a molecular weight of approximately 42 kDa in SDS-PAGE gels. This 42 kDa protein also reacts with a monoclonal antibody specific for the E1 endoglucanase on Western blots, thus confirming its identity as E1 CAT.

Detailed Description Text (42):

Calorimetric studies of the denaturation of the full size E1 enzyme and the proteolytically cleaved E1 CAT were carried at pH 5.0 in 50 mM sodium acetate, using a Microcal MC-2 differential scanning microcalorimeter over a temperature

range of 25.degree.-95.degree. C. and using a scan rate of 20.degree. C./h. For the examples shown in FIG. 2, the protein concentrations were 0.24 mg/mL for the native E1 enzyme and 0.14 mg/mL for E1 CAT.

Detailed Description Paragraph Table (1):

SEQUENCE LISTING (1) GENERAL INFORMATION: (iii) NUMBER OF SEQUENCES: 12 (2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (ix) FEATURE: (A) NAME/KEY: E1-f primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: CTCGAGAAAAGAGCGGGCGGGCTATTGG30 (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein (ix) FEATURE: (A) NAME/KEY: E1-f primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: LeuGluLysArgAlaGlyGlyTyrTrp 510 (2) INFORMATION FOR SEQ ID NO: 3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic Acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (ix) FEATURE: (A) NAME/KEY: E1r (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: CCTAGGTTAACCTTGCTGCGCAGGC24 (2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein (ix) FEATURE: (A) NAME/KEY: E1r (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: SerAlaAlaCysAla (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic Acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: ATTTTCGATCCTGTCTAACATGATCTGCATCGCCTAGC36 (2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: SerSerIlePheAspProValGlyAlaSerAlaSerProSerSerGln 51015 (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: TCGTCGATTTCGATCCTGTCTGGCGCGTCTGCATCGCCTAGCAGTCAA48 (2) INFORMATION FOR SEQ ID NO: 8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (ix) FEATURE: (A) NAME/KEY: mutagenic oligo (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: ATTTTCGATCCTGTCTAACATGATCTGCATCGCCTAGC36 (2) INFORMATION FOR SEQ ID NO: 9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 48 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (ix) FEATURE: (A) NAME/KEY: mutated DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: TCGTCGATTTCGATCCTGTCTAACATGATCTGCATCGCCTAGCAGTCAA48 (2) INFORMATION FOR SEQ ID NO: 10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein (ix) FEATURE: (A) NAME/KEY: Mutated amino acid (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: SerSerIlePheAspProValXaaXaaSerAlaSerProSerSerGln 51015 (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 358 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: Protein (ix) FEATURE: (A) NAME/KEY: E1-CAT (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: AlaGlyGlyGlyTyrTrpHisThrSerGlyArgGluIleLeuAspAla 151015 AsnAsnValProValArgIleAlaGlyIleAsnTrpPheGlyPheGlu 202530 ThrCysAsnTyrValValHisGlyLeuTrpSerArgAspTyrArgSer 354045 MetLeuAspGlnIleLysSerLeuGlyTyrAsnThrIleArgLeuPro 505560 TyrSerAspAspIleLeuLysProGlyThrMetProAsnSerIleAsn 65707580 PheTyrGlnMetAsnGlnAspLeuGlnGlyLeuThrSerLeuGlnVal 859095 MetAspLysIleValAlaTyrAlaGlyGlnIleGlyLeuArgIleIle 100105110 LeuAspArgHisArgProAspCysSerGlyGlnSerAlaLeuTrpTyr 115120125 ThrSerSerValSerGluAlaThrTrpIleSerAspLeuGlnAlaLeu 130135140 AlaGlnArgTyrLysGlyAsnProThrValValGlyPheAspLeuHis 145150155160 AsnGluProHisAspProAlaCysTrpGlyCysGlyAspProSerIle 165170175 AspTrpArgLeuAlaAlaGluArgAlaGlyAsnAlaValLeuSerVal 180185190 AsnProAsnLeuLeuIlePheValGluGlyValGlnSerTyrAsnGly 195200205

AspSerTyrTrpTrpGlyGlyAsnLeuGlnGlyAlaGlyGlnTyrPro 210215220
ValValLeuAsnValProAsnArgLeuValTyrSerAlaHisAspTyr 225230235240
AlaThrSerValTyrProGlnThrTrpPheSerAspProThrPhePro 245250255
AsnAsnMetProGlyIleTrpAsnLysAsnTrpGlyTyrLeuPheAsn 260265270
GlnAsnIleAlaProValTrpLeuGlyGluPheGlyThrThrLeuGln 275280285
SerThrThrAspGlnThrTrpLeuLysThrLeuValGlnTyrLeuArg 290295300
ProThrAlaGlnTyrGlyAlaAspSerPheGlnTrpThrPheTrpSer 305310315320
TrpAsnProAspSerGlyAspThrGlyGlyIleLeuLysAspAspTrp 325330335
GlnThrValAspThrValLysAspGlyTyrLeuAlaProIleLysSer 340345350 SerIlePheAspProVal
355358 (2) INFORMATION FOR SEQ ID NO: 12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH:
2293 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY:
linear (ii) MOLECULE TYPE: DNA (ix) FEATURE: (A) NAME/KEY: E1-CAT (xi) SEQUENCE
DESCRIPTION: SEQ ID NO: 12:
GGATCCACGTTGTACAAGGTACACCTGTCCCGTCGTTCTGGTAGAGCGGGGGATGGTCACC60
CGCACGATCTCTCTTGTGATGTCGACGGTCACGGTTACGGTTGCGCTCGGCCGCG120
ATTTTCGCGCTCGGGCTTGCTCCGGCTGTCGGGTTGGCGTGGTGTGCAGGAC180
GCCGAGGCGATCCAATGAGGGCAAGGGCAAGAGCGGAGCCGATGGCACGTCGGTGGCC240
GATGGGGTACGCCATGGGGCGTGGCGTCCCCGCCGCGAACAGAACGGATGCGGAATAG300
GTCACGGTGCACATGTTGCCGTACCGCGGACCCGGATGACAAGGGTGGGTGCGGGTC360
GCCTGTGAGCTGCCGGCTGGCGTCTGGATCATGGAAACGATCCCACCATCCCCGCAATC420
GACGCGATCAGGGAGCAGGGCGCGAGCCGGACCGTGTGGTCGAGCCGGACGATTGCC480
CATACGGTGCCTGCAATGCCAGCGCCATGTTGTCATGCCAAATGCAATGCACAC540
ATGGACAGGGATTGTGACTCTGAGTAATGATTGGATTGCCCTTGTGCCCTACCGCTTA600
CGCAGAGTAGGCAGCTGTATGCCGTAGGTTGGCGCTCCAGCCGTGGCTGGACATGCCTG660
CTGCGAACTCTTGACACGTCCTGGTTGAAACGCGCAATACTCCAACACCGATGGATCGTT720
CCCATAAGTTCCGTCACAACAGAACGCGCCATGCGCCATGATCAACGTGAAAGGAGT780
ACGGGGGAGAACAGACGGGGGAGAACCAACGGGGGATTGGCGGTGCCGCGCATTGCG840
GCGAGTGCCTGGCTCGCGGGTGTGCTGCGGGTGGCGTGTGCGGGTGTGGCATT900
GGTTGCCGCACTGCCAACCTAGCCGTGCCGCGCCGGCTCGGCCGCCGGCGGGCTA960
TTGGCACACGAGCGCCGGGAGATCCTGGACGCGAACACGGTGCCTGACGGATGCCGG1020
CATCAACTGGTTGGGTTGCAAACTGCAATTACGTCGTGACGGTCTCTGGTCACGCGA1080
CTACCGCAGCATGCTCGACCGAGATAAAGTCGCTCGCTACAACACAATCCGGTGCCTA1140
CTCTGACGACATTCTCAAGCCGGCACCATGCCAACAGCATCAATTACGAGATGAA1200
TCAGGACCTGCAGGGTCTGACGTCCTGCAAGGTGATGGACAAAATCGTCGCGTACGCCGG1260
TCAGATCGGCCTGCGCATCATTCTTGACCGCCACCGACCGGATTGCAAGCGGGCAGTCGGC1320
GCTGTGGTACACGAGCAGCGTCTCGGAGGCTACGTGGATTCCGACCTGCAAGCGCTGGC1380
GCAGCGCTACAAGGGAAACCGACGGTCGTCGGTTGACTGCACAACGAGCCGATGA1440
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CGGAAACGCCGTGCTCTCGGTGAATCCGAAACCTGCTCATTTCGTCGAAGGTGTGCAGAG1560
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CGTGCTGAACGTGCCGAACCGCTGGTGTACTCGCGCACGACTACGGACGAGCGTCA1680
CCCGCAGACGTGGTTGAGCGATCCGACCTCCCCAACACATGCCGGCATCTGGAACAA1740
GAACGGGGATACCTCTCAATCAGAACATTGCAACGGTATGGCTGGCGAATTGGTAC1800
GACACTGCAATCACGACCGACCAGACGTGGCTGAAGACGCTCGTCAACTACGCC1860
GACCGCGCAATACGGTGCAGCAGCTCCAGTGGACCTTCTGGTCTGGAACCCGATT1920
CGGCAGACACAGGAGGAATTCTCAAGGATGACTGGCAGACGGTCGACACAGTAAAGACGG1980
CTATCTCGCGCCGATCAAGTCGTCGATTTGATCCTGCTAATGATCTGCATGCCCTAG2040
CAGTCACCGTCCCCGTGGTGTGCCGTCCCGAGCCGAGCCCCTGGCGAGTCGGAC2100
GCCGACGCCACTCCGACGCCGACAGCCAGCCGACGCCAACGCTGACCCCTACTGCTAC2160
GCCCAACGCCAACGGCAAGCCGACGCCGTCAACGGCAGGCCAGCCTCCGGAGGCCGCTGCAC2220
CGCGAGTTACCAAGGTCAACAGCATTGGGCAATGGCTTCACGGTAACGGTGGCCGTGAC2280 AAATTCCGGATCC2293

CLAIMS:

9. The DNA according to claim 7 wherein the DNA encodes a protein having an endoglucanase activity.

13. The DNA according to claim 2 wherein the DNA encodes a protein having an endoglucanase activity.

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